

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: July 13, 2004, 12:50:24 ; Search time 14.5 seconds

(Without alignments)
53.406 Million cell updates/sec

Title: US-09-830-839-1
Sequence: 1 MTEQWNPAGIENAA 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:*

- 1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/2/1aa/PTUS_COMB.pep:*
- 6: /cgn2_6/prodata/2/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	51	3	US-08-818-112-104 Sequence 104, App
2	79	100.0	51	4	US-08-818-111-99 Sequence 99, Appl
3	79	100.0	51	4	US-09-056-556-104 Sequence 104, App
4	79	100.0	51	4	US-09-072-596-99 Sequence 99, Appl
5	79	100.0	51	4	US-09-072-967-104 Sequence 104, App
6	79	100.0	95	2	US-08-465-640-2 Sequence 2, Appl
7	79	100.0	403	4	US-09-050-739-173 Sequence 173, App
8	79	100.0	404	4	US-09-050-739-172 Sequence 172, App
9	52	65.8	10	3	US-09-001-984C-77 Sequence 77, Appl
10	52	65.8	10	4	US-09-396-347F-77 Sequence 77, Appl
11	42	53.2	409	4	US-09-198-452A-554 Sequence 554, App
12	42	53.2	413	1	US-08-579-667-4 Sequence 4, Appl
13	41	51.9	176	4	US-09-662-842-3 Sequence 3, Appl
14	41	51.9	176	4	US-09-393-171-3 Sequence 3, Appl
15	39	49.4	538	4	US-09-252-991A-18026 Sequence 18026, A
16	39	49.4	928	4	US-09-252-991A-24200 Sequence 24200, A
17	38	48.1	155	3	US-08-685-808-3 Sequence 3, Appl
18	38	48.1	155	3	US-08-505-860C-3 Sequence 3, Appl
19	38	48.1	349	4	US-09-889-039A-13578 Sequence 13578, A
20	38	48.1	410	1	US-08-579-667-2 Sequence 2, Appl
21	38	48.1	410	1	US-08-579-667-6 Sequence 6, Appl
22	38	48.1	410	1	US-08-579-667-8 Sequence 8, Appl
23	38	48.1	795	4	US-09-252-991A-30635 Sequence 30635, A
24	38	48.1	2293	3	US-09-368-590-2 Sequence 2, Appl
25	37	46.8	331	4	US-09-489-039A-9639 Sequence 9639, Ap
26	37	46.8	435	4	US-09-252-991A-23220 Sequence 23220, A
27	37	46.8	493	4	US-09-540-236-2120 Sequence 2120, Ap

28	37	46.8	820	4	US-09-134-000C-6437 Sequence 6437, Ap
29	36.5	46.2	934	1	US-08-215-805A-80 Sequence 80, Appl
30	36	45.6	149	4	US-09-634-238-265 Sequence 265, App
31	36	45.6	149	4	US-09-489-039A-8963 Sequence 8963, Ap
32	36	45.6	221	4	US-09-904-615-155 Sequence 155, App
33	36	45.6	282	4	US-09-724-623-113 Sequence 113, App
34	36	45.6	376	4	US-09-270-957-4 Sequence 4, Appl
35	36	45.6	376	4	US-09-270-957-19 Sequence 19, Appl
36	36	45.6	602	4	US-09-149-727-2 Sequence 2, Appl
37	36	45.6	602	4	US-09-270-957-2 Sequence 2, Appl
38	36	45.6	602	4	US-09-270-957-8 Sequence 8, Appl
39	36	45.6	602	4	US-09-270-957-15 Sequence 15, Appl
40	36	45.6	607	4	US-09-149-727-8 Sequence 8, Appl
41	36	45.6	607	4	US-09-270-957-18 Sequence 18, Appl
42	36	45.6	608	4	US-08-637-670-36 Sequence 36, Appl
43	36	45.6	615	4	US-09-270-957-28 Sequence 28, Appl
44	36	45.6	618	4	US-09-149-727-4 Sequence 4, Appl
45	36	45.6	702	4	US-09-107-532A-5645 Sequence 5645, Ap

ALIGNMENTS

RESULT 1
US-08-818-112-104
Sequence 104, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghon, Raymond
APPLICANT: Veddick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-112-104
Query Match 100.0%; Score 79; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: July 13, 2004, 12:54:00 ; Search time 40 Seconds
(without alignments)

116.969 Million cell updates/sec

Title: US-09-830-839-1

Sequence: 1 MTEQQMFAIGIAAA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1279676 seqs, 311918243 residues

Total number of hits satisfying chosen parameters: 1279676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	15	US-10-079-167-79	Sequence 79, Appl
2	79	100.0	15	US-10-345-000-1	Sequence 1, Appl
3	79	100.0	51	US-09-886-349A-33	Sequence 33, Appl
4	79	100.0	51	US-10-193-002-99	Sequence 99, Appl
5	79	100.0	51	US-10-084-843-104	Sequence 104, Appl
6	79	100.0	51	US-10-098-732A-33	Sequence 33, Appl
7	79	100.0	95	US-09-805-427A-1	Sequence 1, Appl
8	79	100.0	95	US-09-872-505-1	Sequence 1, Appl
9	79	100.0	403	US-09-791-171-173	Sequence 173, Appl
10	79	100.0	403	US-09-805-427A-4	Sequence 4, Appl
11	79	100.0	403	US-09-804-980-173	Sequence 173, Appl
12	79	100.0	403	US-09-872-505-4	Sequence 4, Appl
13	79	100.0	403	US-09-943-443-173	Sequence 173, Appl
14	79	100.0	403	US-10-620-246-173	Sequence 173, Appl
15	79	100.0	404	US-09-791-171-172	Sequence 172, Appl

16	79	100.0	404	US-09-805-427A-3	Sequence 3, Appl
17	79	100.0	404	US-09-804-980-172	Sequence 172, Appl
18	79	100.0	404	US-09-872-505-3	Sequence 3, Appl
19	79	100.0	404	US-09-943-443-172	Sequence 172, Appl
20	79	100.0	404	US-10-620-246-172	Sequence 172, Appl
21	59	74.7	20	US-09-813-333-60	Sequence 60, Appl
22	59	74.7	20	US-10-239-103-60	Sequence 60, Appl
23	59	74.7	20	US-10-044-703-60	Sequence 60, Appl
24	54	68.4	15	US-10-079-167-80	Sequence 80, Appl
25	54	68.4	15	US-10-345-000-2	Sequence 2, Appl
26	48	60.8	893	US-10-282-122A-69721	Sequence 69721, A
27	43	54.4	13	US-09-813-333-59	Sequence 59, Appl
28	43	54.4	13	US-10-239-103-59	Sequence 59, Appl
29	43	54.4	13	US-10-044-703-59	Sequence 59, Appl
30	43	54.4	20	US-09-813-333-61	Sequence 61, Appl
31	43	54.4	20	US-10-239-103-61	Sequence 61, Appl
32	43	54.4	20	US-10-044-703-61	Sequence 61, Appl
33	43	54.4	911	US-10-282-122A-51365	Sequence 51365, A
34	42	53.2	409	US-10-289-762-554	Sequence 554, Appl
35	42	53.2	539	US-10-369-493-16773	Sequence 16773, A
36	41	51.9	176	US-10-339-278-3	Sequence 3, Appl
37	41	51.9	445	US-10-282-122A-76999	Sequence 76999, A
38	40	50.6	295	US-09-738-626-4782	Sequence 4782, Ap
39	40	50.6	939	US-10-282-122A-68011	Sequence 68011, A
40	39	49.4	243	US-10-239-663-39	Sequence 39, Appl
41	39	49.4	288	US-10-369-493-8029	Sequence 8029, Ap
42	39	49.4	498	US-10-425-114-62705	Sequence 62705, A
43	39	49.4	916	US-09-815-242-12006	Sequence 12006, A
44	39	49.4	916	US-10-282-122A-66644	Sequence 66644, A
45	38	48.1	160	US-10-425-114-57412	Sequence 57412, A

ALIGNMENTS

RESULT 1
US-10-079-167-79
Sequence 79, Application US/10079167
Publication No. US20030138454A1
GENERAL INFORMATION:
APPLICANT: Hill, Adrian V.S.
APPLICANT: McShane, Helen C.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Reece, William
TITLE OF INVENTION: Vaccination Method
FILE REFERENCE: 2907.1000-001
CURRENT APPLICATION NUMBER: US/10/079, 167
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 09/454, 204
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: PCT/GB98/01681
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: GB 97 11957.2
PRIOR FILING DATE: 1997-06-09
PRIOR APPLICATION NUMBER: PCT/GB01/04116
PRIOR FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: GB 00 23203.3
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 79
LENGTH: 15
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: T cell epitope in ESAT6
US-10-079-167-79

Query Match 100.0%; Score 79; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using SW model

Run on: July 13, 2004, 12:50:24 ; Search time 14.5 Seconds

(Without alignments)
53.406 Million cell updates/sec

Title: US-09-830-839-6

Sequence: 1 MNFAGIEAASAIQG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patents: AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	51	3	US-08-818-112-104 Sequence 104, App
2	77	100.0	51	4	US-08-818-111-99 Sequence 99, App
3	77	100.0	51	4	US-09-056-556-104 Sequence 104, App
4	77	100.0	51	4	US-09-072-596-99 Sequence 99, App
5	77	100.0	51	4	US-09-072-967-104 Sequence 104, App
6	77	100.0	95	2	US-08-655-640-2 Sequence 2, App
7	77	100.0	403	4	US-09-050-739-173 Sequence 173, App
8	77	100.0	404	4	US-09-050-739-172 Sequence 172, App
9	42.5	55.2	556	4	US-09-252-991A-1793 Sequence 1793, A
10	42	54.5	409	4	US-09-198-452A-554 Sequence 554, App
11	41	53.2	149	4	US-09-634-238-265 Sequence 265, App
12	41	53.2	282	4	US-09-724-623-113 Sequence 113, App
13	40	51.9	2293	3	US-09-368-590-2 Sequence 2, App
14	39	50.6	221	4	US-09-804-615-155 Sequence 155, App
15	39	50.6	413	4	US-09-252-991A-29788 Sequence 29788, A
16	39	50.6	1138	4	US-09-489-039A-13574 Sequence 13574, A
17	38	49.4	185	4	US-09-489-039A-13574 Sequence 13574, A
18	38	49.4	349	4	US-09-489-039A-13578 Sequence 13578, A
19	38	49.4	365	4	US-09-252-991A-30166 Sequence 30166, A
20	38	49.4	418	4	US-09-202-893B-4 Sequence 4, App
21	38	49.4	435	4	US-09-252-991A-21220 Sequence 21220, A
22	37	48.1	209	4	US-09-252-991A-24013 Sequence 24013, A
23	37	48.1	360	4	US-09-252-991A-20838 Sequence 20838, A
24	37	48.1	475	4	US-09-252-991A-21335 Sequence 21335, A
25	37	48.1	947	4	US-09-252-991A-25952 Sequence 25952, A
26	37	48.1	1138	4	US-09-252-991A-25952 Sequence 25952, A
27	36	46.8	294	4	US-09-489-039A-10933 Sequence 10933, A

28	36	46.8	323	4	US-09-489-039A-13907 Sequence 13907, A
29	36	46.8	328	4	US-09-489-039A-10986 Sequence 10986, A
30	36	46.8	368	4	US-09-489-039A-13753 Sequence 13753, A
31	36	46.8	389	4	US-09-489-039A-8540 Sequence 8540, A
32	36	46.8	429	4	US-09-134-000C-3817 Sequence 3817, App
33	36	46.8	483	4	US-09-489-039A-13018 Sequence 13018, A
34	36	46.8	1534	4	US-09-543-681A-5182 Sequence 5182, App
35	35.5	46.1	467	4	US-09-252-991A-29729 Sequence 29729, A
36	35	45.5	29	2	US-08-482-142-11 Sequence 11, App
37	35	45.5	29	2	US-08-482-142-11 Sequence 11, App
38	35	45.5	29	2	US-08-478-572-74 Sequence 74, App
39	35	45.5	29	2	US-08-478-572-74 Sequence 74, App
40	35	45.5	29	3	US-08-484-296-74 Sequence 11, App
41	35	45.5	29	3	US-08-484-296-74 Sequence 11, App
42	35	45.5	29	5	PCT-US95-04481-3 Sequence 74, App
43	35	45.5	117	3	US-09-042-353-232 Sequence 232, App
44	35	45.5	117	4	US-08-758-417A-80 Sequence 80, App
45	35	45.5	159	3	US-09-347-803-18 Sequence 18, App

ALIGNMENTS

RESULT 1
US-08-818-112-104
Sequence 104, Application US/08818112
Patent No. 6280969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, David C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twadzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818.112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-112-104
Query Match 100.0%; Score 77; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2004, 12:54:00 ; Search time 40 Seconds
(without alignments)
116.969 Million cell updates/sec

Title: US-09-830-839-6

Perfect score: 77
Sequence: 1 WNFACIEAASAIQC 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1279676 seqs, 311918243 residues

Total number of hits satisfying chosen parameters: 1279676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	15	14	US-10-079-167-80
2	77	100.0	15	15	US-10-345-000-2
3	77	100.0	20	9	US-09-813-333-60
4	77	100.0	20	12	US-10-239-103-60
5	77	100.0	20	13	US-10-044-703-60
6	77	100.0	51	12	US-09-886-349A-33
7	77	100.0	51	14	US-10-193-002-99
8	77	100.0	51	14	US-10-084-843-104
9	77	100.0	51	14	US-10-096-732A-33
10	77	100.0	95	9	US-09-805-427A-1
11	77	100.0	95	11	US-09-872-505-1
12	77	100.0	403	9	US-09-791-171-173
13	77	100.0	403	9	US-09-805-427A-4
14	77	100.0	403	10	US-09-804-980-173
15	77	100.0	403	11	US-09-872-505-4

16	77	100.0	403	12	US-09-943-443-173	Sequence 173, App
17	77	100.0	403	16	US-10-620-246-173	Sequence 173, App
18	77	100.0	404	9	US-09-791-171-172	Sequence 172, App
19	77	100.0	404	9	US-09-805-427A-3	Sequence 3, Appl1
20	77	100.0	404	10	US-09-804-980-172	Sequence 172, App
21	77	100.0	404	11	US-09-872-505-3	Sequence 3, Appl1
22	77	100.0	404	12	US-09-943-443-172	Sequence 172, App
23	77	100.0	404	16	US-10-620-246-172	Sequence 172, App
24	66	85.7	20	9	US-09-813-333-61	Sequence 61, Appl
25	66	85.7	20	12	US-10-239-103-61	Sequence 61, Appl
26	66	85.7	20	13	US-10-044-703-61	Sequence 61, Appl
27	60	77.9	13	9	US-09-813-333-59	Sequence 59, Appl
28	60	77.9	13	12	US-10-239-103-59	Sequence 59, Appl
29	60	77.9	13	13	US-10-044-703-59	Sequence 59, Appl
30	54	70.1	15	14	US-10-079-167-79	Sequence 79, Appl
31	54	70.1	15	15	US-10-345-000-1	Sequence 79, Appl
32	43	55.8	400	15	US-10-369-493-21850	Sequence 21850, A
33	42.5	55.2	141	12	US-10-389-647-560	Sequence 560, App
34	42	54.5	409	15	US-10-289-762-554	Sequence 554, App
35	42	54.5	1447	16	US-10-437-963-133273	Sequence 133273, App
36	41	53.2	93	16	US-10-437-963-108079	Sequence 108079, App
37	41	53.2	149	15	US-10-264-213-168	Sequence 168, App
38	41	53.2	282	14	US-10-288-930-113	Sequence 113, App
39	41	53.2	443	15	US-10-369-493-9058	Sequence 9058, App
40	41	53.2	445	12	US-10-282-122A-76999	Sequence 76999, A
41	41	53.2	463	14	US-10-156-761-12653	Sequence 12653, A
42	41	53.2	528	12	US-10-282-122A-50764	Sequence 50764, A
43	41	53.2	893	12	US-10-282-122A-69721	Sequence 69721, A
44	40	51.9	419	16	US-10-437-963-168592	Sequence 168592, A
45	40	51.9	934	16	US-10-437-963-164110	Sequence 164110, A

ALIGNMENTS

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APPLICANT: Schneider, Joerg
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OTHER INFORMATION: T cell epitope in ESAT6
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Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;